

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Dalla-Favera, Riccardo
Chaganti, Raju S.K.
- (ii) TITLE OF INVENTION: CLONING AND USES OF THE GENETIC LOCUS
bcl-6
- (iii) NUMBER OF SEQUENCES: 9
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Cooper & Dunham LLP
 - (B) STREET: 1185 Avenue of the Americas
 - (C) CITY: New York
 - (D) STATE: New York
 - (E) COUNTRY: United States of America
 - (F) ZIP: 10036
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: White, John P.
 - (B) REGISTRATION NUMBER: 28,678
 - (C) REFERENCE/DOCKET NUMBER: 0575/43771-A-PCT-US-Y
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (212) 278-0400
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 - (C) TELEX: 422523 COOP UI

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3720 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 328..2445
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGCCCCTCGA	GCCTCGAACC	GGAACCTCCA	AATCCGAGAC	GCTCTGCTTA	TGAGGACCTC	60
GAAATATGCC	GGCCAGTGAA	AAAATCTTAT	GGCTTTGAGG	GCTTTTG GTT	GGCCAGGGGC	120

AGTAAAAATC TCGGAGAGCT GACACCAAGT CCTCCCTGTC CACGTAGCAG TGGTAAAGTC	180
CGAAGCTCAA ATTCCGAGAA TTGAGCTCTG TTGATTCTTA GAACTGGGGT TCTTAGAAGT	240
GGTGATGCAA GAAGTTTCTA GGAAAGGCCG GACACCAGGT TTTGAGCAAA ATTTTGGACT	300
GTGAAGCAAG GCATIGGTGA AGACAAA ATG GCC TCG CCG GCT GAC AGC TGT Met Ala Ser Pro Ala Asp Ser Cys 1 5	351
ATC CAG TTC ACC CGC CAT GCC AGG GAT GTT CTT CTC AAC CTT AAT CGT Ile Gln Phe Thr Arg His Ala Arg Asp Val Leu Leu Asn Leu Asn Arg 10 15 20	399
CTC CGG AGT CGA GAC ATC TTG ACT GAT GTT GTC ATT GTT GTG AGC CGT Leu Arg Ser Arg Asp Ile Leu Thr Asp Val Val Ile Val Val Ser Arg 25 30 35 40	447
GAG CAG TTT AGA GCC CAT AAA ACG GTC CTC ATG GCC TGG AGA GGC CTG Glu Gln Phe Arg Ala His Lys Thr Val Leu Met Ala Trp Arg Gly Leu 45 50 55	495
TTC TAT AGC ATC TTT ACA GAC CAG TTG AAA TGC AAC CTT AGT GTG ATC Phe Tyr Ser Ile Phe Thr Asp Gln Leu Lys Cys Asn Leu Ser Val Ile 60 65 70	543
AAT CTA GAT CCT GAG ATC AAC CCT GAG GGA TTC TGC ATC CTC CTG GAC Asn Leu Asp Pro Glu Ile Asn Pro Glu Gly Phe Cys Ile Leu Leu Asp 75 80 85	591
TTC ATG TAC ACA TCT CGG CTC AAT TTG CGG GAG GGC AAC ATC ATG GCT Phe Met Tyr Thr Ser Arg Leu Asn Leu Arg Glu Gly Asn Ile Met Ala 90 95 100	639
GTG ATG GCC ACG GCT ATG TAC CTG CAG ATG GAG CAT GTT GTG GAC ACT Val Met Ala Thr Ala Met Tyr Leu Gln Met Glu His Val Val Asp Thr 105 110 115 120	687
TGC CGG AAG TTT ATT AAG GCC AGT GAA GCA GAG ATG GTT TCT GCC ATC Cys Arg Lys Phe Ile Lys Ala Ser Glu Ala Glu Met Val Ser Ala Ile 125 130 135	735
AAG CCT CCT CGT GAA GAG TTC CTC AAC AGC CGG ATG CTG ATG CCC CAA Lys Pro Pro Arg Glu Glu Phe Leu Asn Ser Arg Met Leu Met Pro Gln 140 145	783
GAC ATC ATG GCC TAT CGG GGT CGT GAG GTG GTG GAG AAC AAC CTG CCA Asp Ile Met Ala Tyr Arg Gly Arg Glu Val Val Glu Asn Asn Leu Pro 155 160 165	831
CTG AGG AGC GCC CCT GGG TGT GAG AGC AGA GCC TTT GCC CCC AGC CTG Leu Arg Ser Ala Pro Gly Cys Glu Ser Arg Ala Phe Ala Pro Ser Leu 170 175 180	879
TAC AGT GGC CTG TCC ACA CCG CCA GCC TCT TAT TCC ATG TAC AGC CAC Tyr Ser Gly Leu Ser Thr Pro Pro Ala Ser Tyr Ser Met Tyr Ser His 185 190 195 200	927
CTC CCT GTC AGC AGC CTC CTC TTC TCC GAT GAG GAG TTT CGG GAT GTC Leu Pro Val Ser Ser Leu Leu Phe Ser Asp Glu Glu Phe Arg Asp Val 205 210 215	975

CGG ATG CCT GTG GCC AAC CCC TTC CCC AAG GAG CGG GCA CTC CCA TGT Arg Met Pro Val Ala Asn Pro Phe Pro Lys Glu Arg Ala Leu Pro Cys 220 225 230	1023
GAT AGT GCC AGG CCA GTC CCT GGT GAG TAC AGC CGG CCG ACT TTG GAG Asp Ser Ala Arg Pro Val Pro Gly Glu Tyr Ser Arg Pro Thr Leu Glu 235 240 245	1071
GTG TCC CCC AAT GTG TGC CAC AGC AAT ATC TAT TCA CCC AAG GAA ACA Val Ser Pro Asn Val Cys His Ser Asn Ile Tyr Ser Pro Lys Glu Thr 250 255 260	1119
ATC CCA GAA GAG GCA CGA AGT GAT ATG CAC TAC AGT GTG GCT GAG GGC Ile Pro Glu Glu Ala Arg Ser Asp Met His Tyr Ser Val Ala Glu Gly 265 270 275 280	1167
CTC AAA CCT GCT GCC CCC TCA GCC CGA AAT GCC CCC TAC TTC CCT TGT Leu Lys Pro Ala Ala Pro Ser Ala Arg Asn Ala Pro Tyr Phe Pro Cys 285 290 295	1215
GAC AAG GCC AGC AAA GAA GAA GAG AGA CCC TCC TCG GAA GAT GAG ATT Asp Lys Ala Ser Lys Glu Glu Glu Arg Pro Ser Ser Glu Asp Glu Ile 300 305 310	1263
GCC CTG CAT TTC GAG CCC CCC AAT GCA CCC CTG AAC CGG AAG GGT CTG Ala Leu His Phe Glu Pro Pro Asn Ala Pro Leu Asn Asp Lys Gly Leu 315 320 325	1311
GTT AGT CCA CAG AGC CCC CAG AAA TCT GAC TGC CAG CCC AAC TCG CCC Val Ser Pro Gln Ser Pro Gln Lys Ser Asp Cys Gln Pro Asn Ser Pro 330 335 340	1359
ACA GAG GCC TGC AGC AGT AAG AAT GCC TGC ATC CTC CAG GGT TCT GGC Thr Glu Ala Cys Ser Ser Lys Asn Ala Cys Ile Leu Gln Gly Ser Gly 345 350 355 360	1407
TCC CCT CCA GCC AAG AGC CCC ACT GAC CCC AAA GCC TGC AGC TGG AAG Ser Pro Pro Ala Lys Ser Pro Thr Asp Pro Lys Ala Cys Ser Trp Lys 365 370 375	1455
AAA TAC AAG TTC ATC GTG CTC AAC AGC CTC AAC CAG AAT GCC AAA CCA Lys Tyr Lys Phe Ile Val Leu Asn Ser Ser Leu Asn Gln Asn Ala Lys Pro 380 385 390	1503
GGG GGG CCT GAG CAG GCT GAG CTG GGC CGC CTT TCC CCA CGA GCC TAC Gly Gly Pro Glu Gln Ala Glu Leu Gly Arg Leu Ser Pro Arg Ala Tyr 395 400 405	1551
ACG GCC CCA CCT GCC TGC CAG CCA CCC ATG GAG CCT GAG AAC CTT GAC Thr Ala Pro Pro Ala Cys Gln Pro Pro Met Glu Glu Glu Asn Leu Asp 410 415 420	1599
CTC CAG TCC CCA ACC AAG CTG AGT GCC AGC GGG GAG GAC TCC ACC ATC Leu Gln Ser Pro Thr Lys Leu Ser Ala Ser Gly Glu Asp Ser Thr Ile 425 430 435 440	1647
CCA CAA GCC AGC CGG CTC AAT AAC ATC GTT AAC AGG TCC ATG ACG GGC Pro Gln Ala Ser Arg Leu Asn Asn Ile Val Asn Arg Ser Met Thr Gly 445 450 455	1695
TCT CCC CGC AGC AGC AGC GAG AGC CAC TCA CCA CTC TAC ATG CAC CCC Ser Pro Arg Ser Ser Ser Glu Ser His Ser Pro Leu Tyr Met His Pro 460 465 470	1743

460															465															470															
CCG Pro	AAG Lys	TGC Cys 475	ACG Thr	TCC Ser	TGC Cys	GGC Gly	TCT Ser 480	CAG Gln	TCC Ser	CCA Pro	CAG Gln	CAT His 485	GCA Ala	GAG Glu	ATG Met	1791																													
TGC Cys	CTC Leu 490	CAC His	ACC Thr	GCT Ala	GGC Gly	CCC Pro 495	ACG Thr	TTC Phe	GCT Ala	GAG Glu	GAG Pro 500	ATG Met	GGA Gly	GAG Glu	ACC Thr	1839																													
CAG Gln 505	TCT Ser	GAG Glu	TAC Tyr	TCA Ser	GAT Asp 510	TCT Ser	AGC Ser	TGT Cys	GAG Glu	AAC Ser 515	GGG Gly	GCC Ala	TTC Phe	TTC Phe	TGC Cys 520	1889																													
AAT Asn	GAG Glu	TGT Cys	GAC Asp	TGC Cys 525	CGC Arg	TTC Phe	TCT Ser	GAG Glu	GAG Glu 530	GCC Ala	TCA Ser	CTC Leu	AAG Lys	AGG Arg 535	CAC His	1935																													
ACG Thr	CTG Leu	CAG Gln	ACC His 540	CAC His	AGT Ser	GAC Asp	AAA Lys	CCC Pro 545	TAC Tyr	AAG Lys	TGT Cys	GAC Asp	CGC Arg 550	TGC Cys	CAG Gln	1983																													
GCC Ala	TCC Ser	TTC Phe 555	CGC Arg	TAC Tyr	AAG Lys	GGC Gly	AAC Leu 560	CTC Leu	GCC Ala	AGC His	CAC His	AAG Lys 565	ACC Thr	GTC Val	CAT His	2031																													
ACC Thr	GGT Gly 570	GAG Glu	AAA Lys	CCC Pro	TAT Tyr	CGT Arg 575	TGC Cys	AAC Asn	ATC Ile	TGT Gly 580	GGG Gly	GCC Ala	CAG Gln	TTC Phe	AAC Asn	2079																													
CGG Arg 585	CCA Pro	GCC Ala	AAC Asn	CTG Leu	AAA Lys 590	ACC Thr	CAC His	ACT Thr	CGA Arg	ATT Ile 595	CAC His	TCT Ser	GGA Gly	GAG Glu	AAG Lys 600	2127																													
CCC Pro	TAC Lys	AAA Glu 605	TGC Glu	GAA Thr	ACC Cys	TGC Gly	GGA Gly 610	AGC Ala	AGA Arg 610	TTT Phe	GTA Val	CAG Gln	GTG Ala 615	GCC Ala	CAC His	2175																													
CTC Leu	CGT Arg	GCC Ala 620	CAT His	GTG Val	CTT Leu	ATC Ile	CAC His 625	ACT Thr	GGT Gly	GAG Glu	AAG Lys	CCC Pro	TAT Tyr 630	CCC Pro	TGT Cys	2223																													
GAA Glu	ATC Ile 635	TGT Cys	ACC Gly	ACC Thr	CGT Arg	TTC Phe	CGG Arg 640	CAC His	CTT Leu	CAG Gln	ACT Thr	CTG Leu 645	AGC Lys	AGC Ser	CAC His	2271																													
CTG Leu	CGA Arg 650	CAC Ile	ACA His	GGA Gly	GAG Glu 655	AAA Lys	CCT Pro	TAC Tyr	CAT His	TGT Cys 660	GAG Glu	AAG Lys	TGT Cys	AAC Asn	2319																														
CTG Leu 665	CAT His	TTC Phe	CGT Arg	CAC His	AAA Lys 670	ACC Ser	CAG Gln	CTG Leu	CGA Arg	CTT Leu 675	CAC His	TTG Leu	CGC Arg	CAG Gln 680	AAG Lys	2367																													
CAT His	GGC Gly	GCC Ala	ATC Ile	ACC Thr 685	AAC Asn	ACC Thr	AAG Lys	GTG Val	CAA Gln 690	TAC Tyr	CGC Arg	GTG Val	TCA Ser	GCC Ala 695	ACT Thr	2415																													
GAC Asp	CTG Leu	CCT Pro	CCG Pro 700	GAG Glu	CTC Leu	CCC Pro	AAA Lys	GCC Ala 705	TGC Cys	TGAAGCATGG	AGTGTGATG					2465																													

CTTTCGCTCTC CAGCCCCCTTC TCAGAATCTA CCCAAAGGAT ACTGTAACAC TTTACAATGT	2525
TCATCCCATG ATGTAGTGCC TCTTTCATCC ACTAGTGCAA ATCATAGCTG GGGGTGGGG	2585
GTGGTGGGG TCGGGGCTG GGGGACTGGG AGCGCAGCA GCTCCCCCTC CCCCCTGCC	2645
ATAAAACATT AAGAAATCA TATTGCTTCT TCTCCTATGT GNNNNNNNNN NNNNNNNNNN	2705
NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN	2765
NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN	2825
NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN	2885
NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN	2945
NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN	3005
NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN	3065
NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN	3125
NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN	3185
NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN	3245
NTTTAAGTAT TGCACTCTGA TAAGTAAGAA AATATTTTGT CTAATAATGCC TCAGTGATAT	3305
TGTATTTTTT TGCAAGTGGG GGGTTACAAT TTACCCAGTG TGTATTAAAA AAAACCCAAA	3365
GAACCCAAAA ATCTCCAGAA GGAAAAATGT GTAATTTTGT TCTAGTTTTC AGTTTGATATA	3425
TACCCGTACA ACGTGTCCTC ACGGTGCCTT TTTTCAAGGA AGTTTTCATAT GATGGGCGAG	3485
CGTGACCATC CCCTTTTGA AGTGAGTGGCA GACACAGGGA CTTGAAGTTG TTACTAACTA	3545
AACTCTCTTT GGGAAATGTT GTCTCATCCC ANCTGCGCTC ATGCTTGTGT GATAACTACT	3605
CCGGAGACAG GGTTTGGCTG TGTCTAAACT GCATTACCGC GTTGTAAGAA ATAGCTGTAC	3665
CAATATAAGA ATAAAATGTT GGAAAGTCGC AAAAAAAAAA AAAAAAAAAA AAAAA	3720

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 706 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Ser Pro Ala Asp Ser Cys Ile Gln Phe Thr Arg His Ala Arg	
1 5 10 15	
Asp Val Leu Leu Asn Leu Asn Arg Leu Arg Ser Arg Asp Ile Leu Thr	
20 25 30	
Asp Val Val Ile Val Val Ser Arg Glu Gln Phe Arg Ala His Lys Thr	
35 40 45	

Val Leu Met Ala Trp Arg Gly Leu Phe Tyr Ser Ile Phe Thr Asp Gln
50 55 60

Leu Lys Cys Asn Leu Ser Val Ile Asn Leu Asp Pro Glu Ile Asn Pro
65 70 75 80

Glu Gly Phe Cys Ile Leu Leu Asp Phe Met Tyr Thr Ser Arg Leu Asn
85 90 95

Leu Arg Glu Gly Asn Ile Met Ala Val Met Ala Thr Ala Met Tyr Leu
100 105 110

Gln Met Glu His Val Val Asp Thr Cys Arg Lys Phe Ile Lys Ala Ser
115 120 125

Glu Ala Glu Met Val Ser Ala Ile Lys Pro Pro Arg Glu Glu Phe Leu
130 135 140

Asn Ser Arg Met Leu Met Pro Gln Asp Ile Met Ala Tyr Arg Gly Arg
145 150 155 160

Glu Val Val Glu Asn Asn Leu Pro Leu Arg Ser Ala Pro Gly Cys Glu
165 170 175

Ser Arg Ala Phe Ala Pro Ser Leu Tyr Ser Gly Leu Ser Thr Pro Pro
180 185 190

Ala Ser Tyr Ser Met Tyr Ser His Leu Pro Val Ser Ser Leu Leu Phe
195 200 205

Ser Asp Glu Glu Phe Arg Asp Val Arg Met Pro Val Ala Asn Pro Phe
210 215 220

Pro Lys Glu Arg Ala Leu Pro Cys Asp Ser Ala Arg Pro Val Pro Gly
225 230 235 240

Glu Tyr Ser Arg Pro Thr Leu Glu Val Ser Pro Asn Val Cys His Ser
245 250 255

Asn Ile Tyr Ser Pro Lys Glu Thr Ile Pro Glu Glu Ala Arg Ser Asp
260 265 270

Met His Tyr Ser Val Ala Glu Gly Leu Lys Pro Ala Ala Pro Ser Ala
275 280 285

Arg Asn Ala Pro Tyr Phe Pro Cys Asp Lys Ala Ser Lys Glu Glu Glu
290 295 300

Arg Pro Ser Ser Glu Asp Glu Ile Ala Leu His Phe Glu Pro Pro Asn
305 310 315 320

Ala Pro Leu Asn Arg Lys Gly Leu Val Ser Pro Gln Ser Pro Gln Lys
325 330 335

Ser Asp Cys Gln Pro Asn Ser Pro Thr Glu Ala Cys Ser Ser Lys Asn
340 345 350

Ala Cys Ile Leu Gln Gly Ser Gly Ser Pro Pro Ala Lys Ser Pro Thr
355 360 365

Asp Pro Lys Ala Cys Ser Trp Lys Lys Tyr Lys Phe Ile Val Leu Asn

370	375	380
Ser Leu Asn Gln Asn Ala Lys Pro Gly Gly Pro Glu Gln Ala Glu Leu		
385	390	395
Gly Arg Leu Ser Pro Arg Ala Tyr Thr Ala Pro Pro Ala Cys Gln Pro		
	405	410
Pro Met Glu Pro Glu Asn Leu Asp Leu Gln Ser Pro Thr Lys Leu Ser		
	420	425
Ala Ser Gly Glu Asp Ser Thr Ile Pro Gln Ala Ser Arg Leu Asn Asn		
	435	440
Ile Val Asn Arg Ser Met Thr Gly Ser Pro Arg Ser Ser Ser Glu Ser		
	450	455
His Ser Pro Leu Tyr Met His Pro Pro Lys Cys Thr Ser Cys Gly Ser		
	465	470
Gln Ser Pro Gln His Ala Glu Met Cys Leu His Thr Ala Gly Pro Thr		
	485	490
Phe Ala Glu Glu Met Gly Glu Thr Gln Ser Glu Tyr Ser Asp Ser Ser		
	500	505
Cys Glu Asn Gly Ala Phe Phe Cys Asn Glu Cys Asp Cys Arg Phe Ser		
	515	520
Glu Glu Ala Ser Leu Lys Arg His Thr Leu Gln Thr His Ser Asp Lys		
	530	535
Pro Tyr Lys Cys Asp Arg Cys Gln Ala Ser Phe Arg Tyr Lys Gly Asn		
	545	550
Leu Ala Ser His Lys Thr Val His Thr Gly Glu Lys Pro Tyr Arg Cys		
	565	570
Asn Ile Cys Gly Ala Gln Phe Asn Arg Pro Ala Asn Leu Lys Thr His		
	580	585
Thr Arg Ile His Ser Gly Glu Lys Pro Tyr Lys Cys Glu Thr Cys Gly		
	595	600
Ala Arg Phe Val Gln Val Ala His Leu Arg Ala His Val Leu Ile His		
	610	615
Thr Gly Glu Lys Pro Tyr Pro Cys Glu Ile Cys Gly Thr Arg Phe Arg		
	625	630
His Leu Gln Thr Leu Lys Ser His Leu Arg Ile His Thr Gly Glu Lys		
	645	650
Pro Tyr His Cys Glu Lys Cys Asn Leu His Phe Arg His Lys Ser Gln		
	660	665
Leu Arg Leu His Leu Arg Gln Lys His Gly Ala Ile Thr Asn Thr Lys		
	675	680
Val Gln Tyr Arg Val Ser Ala Thr Asp Leu Pro Pro Glu Leu Pro Lys		
	690	695
		700

Ala Cys
705

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 103 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Asp	Gly	Ser	Phe	Val	Gln	His	Ser	Val	Arg	Val	Leu	Gln	Glu	Leu	Asn
1				5						10				15	
Lys	Gln	Arg	Glu	Lys	Gly	Gln	Tyr	Cys	Asp	Ala	Thr	Leu	Asp	Val	Gly
			20					25					30		
Gly	Leu	Val	Phe	Lys	Ala	His	Trp	Ser	Val	Leu	Ala	Cys	Cys	Ser	His
		35					40					45			
Phe	Phe	Gln	Ser	Leu	Tyr	Gly	Asp	Gly	Ser	Gly	Gly	Ser	Val	Val	Leu
			50				55				60				
Pro	Ala	Gly	Phe	Ala	Glu	Ile	Phe	Gly	Leu	Leu	Asp	Phe	Phe	Tyr	
65					70					75				80	
Thr	Gly	His	Leu	Ala	Leu	Thr	Ser	Gly	Asn	Arg	Asp	Gln	Val	Leu	Leu
			85						90					95	
Ala	Ala	Arg	Glu	Leu	Arg	Val									
						100									

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 107 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Asp	Thr	Ala	Ser	His	Ser	Leu	Val	Leu	Leu	Gln	Gln	Leu	Asn	Met
1				5						10				15	
Gln	Arg	Glu	Phe	Gly	Phe	Leu	Cys	Asp	Cys	Thr	Val	Ala	Ile	Gly	Asp
		20						25					30		

Val Tyr Phe Lys Ala His Arg Ala Val Leu Ala Ala Phe Ser Asn Tyr
 35 40 45
 Phe Lys Met Ile Phe Ile His Gln Thr Ser Glu Cys Ile Lys Ile Gln
 50 55 60
 Pro Thr Asp Ile Gln Pro Asp Ile Phe Ser Tyr Leu Leu His Ile Met
 65 70 75 80
 Tyr Thr Gly Lys Gly Pro Lys Gln Ile Val Asp His Ser Arg Leu Glu
 85 90 95
 Glu Gly Ile Arg Phe Leu His Ala Asp Tyr Leu
 100 105

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 106 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Asn Asn Ser Ser Glu Leu Ile Ala Val Ile Asn Gly Phe Arg Asn
 1 5 10 15
 Ser Gly Arg Phe Cys Asp Ile Ser Ile Val Ile Asn Asp Glu Arg Ile
 20 25 30
 Asn Ala His Lys Leu Ile Leu Ser Gly Ala Ser Glu Tyr Phe Ser Ile
 35 40 45
 Leu Phe Ser Asn Asn Phe Ile Asp Ser Asn Glu Tyr Glu Val Asn Leu
 50 55 60
 Ser His Leu Asp Tyr Gln Ser Val Asn Asp Leu Ile Asp Tyr Ile Tyr
 65 70 75 80
 Gly Ile Pro Leu Ser Leu Thr Asn Asp Asn Val Lys Tyr Ile Leu Ser
 85 90 95
 Thr Ala Asp Phe Leu Gln Ile Gly Ser Ala
 100 105

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 108 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```

Cys Leu Arg Trp Asn Asn His Gln Ser Asn Leu Leu Ser Val Phe Asp
 1             5             10             15
Gln Leu Leu His Ala Glu Thr Phe Thr Asp Val Thr Leu Ala Val Glu
      20             25             30
Gly Gln His Leu Lys Ala His Lys Asn Val Leu Ser Ala Cys Ser Pro
      35             40             45
Tyr Phe Asn Thr Leu Phe Val Ser His Pro Glu Lys His Pro Ile Val
      50             55             60
Ile Leu Lys Asp Val Pro Tyr Ser Asp Met Lys Ser Leu Leu Asp Phe
      65             70             75             80
Met Tyr Arg Gly Glu Val Ser Val Asp Gln Glu Arg Leu Thr Ala Phe
      85             90             95
Leu Arg Val Ala Glu Ser Leu Arg Ile Lys Gly Leu
      100             105

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(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```

Gln Tyr Ser Asn Glu Gln His Thr Ala Arg Ser Phe Asp Ala Met Asn
 1             5             10             15
Glu Met Arg Lys Gln Lys Gln Leu Cys Asp Val Ile Leu Val Ala Asp
      20             25             30
Asp Val Glu Ile His Ala His Arg Met Val Leu Ala Ser Cys Ser Pro
      35             40             45
Tyr Phe Tyr Ala Met Phe Thr Ser Phe Glu Glu Ser Arg Gln Ala Arg
      50             55             60
Ile Thr Leu Gln Ser Val Asp Ala Arg Ala Leu Glu Leu Leu Ile Asp
      65             70             75             80
Tyr Val Tyr Thr Ala Thr Val Glu Val Asn Glu Asp Asn Val Gln Val
      85             90             95
Leu Leu Thr Ala Ala Asn Leu Leu Gln Leu Thr Asp Val
      100             105

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(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 105 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

```

Gln Leu Gln Asn Pro Ser His Pro Thr Gly Leu Leu Cys Lys Ala Asn
 1          5          10          15
Gln Met Arg Leu Ala Gly Thr Leu Cys Asp Val Val Ile Met Val Asp
          20          25          30
Ser Gln Glu Phe His Ala His Arg Thr Val Leu Ala Cys Thr Ser Lys
          35          40          45
Met Phe Glu Ile Leu Phe His Arg Asn Ser Gln His Tyr Thr Leu Asp
          50          55          60
Phe Leu Ser Pro Lys Thr Phe Gln Gln Ile Leu Glu Tyr Ala Tyr Thr
          65          70          75          80
Ala Thr Leu Gln Ala Lys Ala Glu Asp Leu Asp Asp Leu Leu Tyr Ala
          85          90          95
Ala Glu Ile Leu Glu Ile Glu Tyr Leu
          100          105
  
```

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 110 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

```

Cys Leu Gln Phe Thr Arg His Ala Ser Asp Val Leu Leu Asn Leu Asn
 1          5          10          15
Arg Leu Arg Ser Arg Asp Ile Leu Thr Asp Val Val Ile Val Val Ser
          20          25          30
Arg Glu Gln Phe Arg Ala His Lys Thr Val Leu Met Ala Cys Ser Gly
          35          40          45
Leu Phe Tyr Ser Ile Phe Thr Asp Gln Leu Lys Cys Asn Leu Ser Val
          50          55          60
  
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-12-

Ile Asn Leu Asp Pro Glu Ile Asn Pro Glu Gly Phe Cys Ile Leu Leu
65 70 75 80

Asp Phe Met Tyr Thr Ser Arg Leu Asn Leu Arg Glu Gly Asn Ile Met
85 90 95

Ala Val Met Ala Thr Ala Met Tyr Leu Gln Met Glu His Val
100 105 110